

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> SPFl-Related Transcription Factors

<130> BB1436 PCT

<140>

<141>

<150> 60/174325

<151> 2000-01-04

<160> 14

<170> Microsoft Office 97

<210> 1

<211> 512

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (368)

<220>

<221> unsure

<222> (387)

<220>

<221> unsure

<222> (405)

<220>

<221> unsure

<222> (408)

<220>

<221> unsure

<222> (445)

<220>

<221> unsure

<222> (447)

<220>

<221> unsure

<222> (453)

<220>

<221> unsure

<222> (462)

<220>

<221> unsure

<222> (489) .. (490) .. (491)

<220>

<221> unsure

<222> (500)

<400> 1

```

ctataattgg cgcaaatatg gacagaagca tgtcaaggga agtgaaaatc ctagaagtta 60
ttacaagtgc actcattccta attgtgaagt taaaaagcta ttagagcggt cgcttgatgg 120
tcagattact gaagttgttt ataaagggca tcataatcat cccaagcccc aaccaaatag 180
aaggtttagct gctgggtgcag ttcccttcaag ccaggctgaa gaaagatacg atgggtgtggc 240
acctattgaa gacaaaacctt caaatattta ttccaacctc tgtaaccaag cacattcagc 300
tggcatgggt gataatgttc cgggtccagc aagtgatgat gatgttgatg ctggaggtgg 360
aagaccnacc cctgggggga tgactcnaat gatgatgatg acttnggnct caaaaacgca 420
aggaaaaatgg aatctgccgg gtatncnatg ccnggctttg antggggtaa accaaatccc 480
ggagccccnn ntcccttttn aaaaactgtt tt 512

```

<210> 2

<211> 170

<212> PRT

<213> Zea mays

<220>

<221> UNSURE

<222> (123)

<220>

<221> UNSURE

<222> (129)

<220>

<221> UNSURE

<222> (135)..(136)

<220>

<221> UNSURE

<222> (148)..(149)

<220>

<221> UNSURE

<222> (151)

<220>

<221> UNSURE

<222> (154)

<220>

<221> UNSURE

<222> (163)..(164)

<220>

<221> UNSURE

<222> (167)

<400> 2

```

Tyr Asn Trp Arg Lys Tyr Gly Gln Lys His Val Lys Gly Ser Glu Asn
  1             5             10             15

```

```

Pro Arg Ser Tyr Lys Cys Thr His Pro Asn Cys Glu Val Lys Lys
      20             25             30

```

Leu Leu Glu Arg Ser Leu Asp Gly Gln Ile Thr Glu Val Val Tyr Lys
 35 40 45
 Gly His His Asn His Pro Lys Pro Gln Pro Asn Arg Arg Leu Ala Ala
 50 55 60
 Gly Ala Val Pro Ser Ser Gln Ala Glu Glu Arg Tyr Asp Gly Val Ala
 65 70 75 80
 Pro Ile Glu Asp Lys Pro Ser Asn Ile Tyr Ser Asn Leu Cys Asn Gln
 85 90 95
 Ala His Ser Ala Gly Met Val Asp Asn Val Pro Gly Pro Ala Ser Asp
 100 105 110
 Asp Asp Val Asp Ala Gly Gly Gly Arg Pro Xaa Pro Gly Gly Met Thr
 115 120 125
 Xaa Met Met Met Met Thr Xaa Xaa Ser Lys Thr Gln Gly Lys Trp Asn
 130 135 140
 Leu Pro Gly Xaa Xaa Cys Xaa Ala Leu Xaa Gly Val Asn Gln Ile Pro
 145 150 155 160
 Glu Pro Xaa Xaa Pro Phe Xaa Lys Leu Phe
 165 170

<210> 3
 <211> 717
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (11)

<220>
 <221> unsure
 <222> (15)

<220>
 <221> unsure
 <222> (610)

<220>
 <221> unsure
 <222> (640)

<220>
 <221> unsure
 <222> (653)

<220>
 <221> unsure
 <222> (680)

<220>
 <221> unsure
 <222> (692)

<220>

<221> unsure

<222> (703)

<400> 3

```

gacgcacccc ntctntttctc tccccctctc gtctcgtcca gtcgtccccc tctccccac 60
tctaccacgc tgccctgctc tgcgtcgtc gccatggcgt cctccacggg gagcttggag 120
cacggggggg tcaagtacac gccgccgccc ttcacacac ccttcaccga gctgctctcc 180
ggcgaggggg acatgctagg agccggcgcc gatcaggagc ggtcgtcgcc gagggggctg 240
ttccaccgcg gcgccagggg cgtgcccaag ttcaagtcgg cgcagcctcc cagcctgccc 300
atctcgccgc cgcccatgtc gccttctctc tacttcgcca tcccgcccg gctcagcccc 360
gccgagctgc tcgactcgcc cgtcctgctc cactcgtcct ccaacatcct ggctgtctcc 420
accactggcg ccatcccgcc gcagaggttc gactggaaga aggcgcgcga cctgatcgcg 480
tctcagtctc agcaagacgg cgacagccgg gctgccgccc ccggttcga cgacttctcc 540
ttcacacggg caccttcaac gccgtgcgcg cgcacacgac gacgacgtcc ttaccttcat 600
gaagaagaan gtggagaggg cctggccga cgggcgcatt aacgcaaat cngtacaata 660
ggcgcgccac aaacaaccn aagccggtg tncacgcgcc ggnaacttaa ttccgga 717

```

<210> 4

<211> 150

<212> PRT

<213> Zea mays

<400> 4

```

Met Ala Ser Ser Thr Gly Ser Leu Glu His Gly Gly Phe Thr Phe Thr
  1              5              10              15

Pro Pro Pro Phe Ile Thr Ser Phe Thr Glu Leu Leu Ser Gly Ala Gly
      20              25              30

Asp Met Leu Gly Ala Gly Ala Asp Gln Glu Arg Ser Ser Pro Arg Gly
      35              40              45

Leu Phe His Arg Gly Ala Arg Gly Val Pro Lys Phe Lys Ser Ala Gln
      50              55              60

Pro Pro Ser Leu Pro Ile Ser Pro Pro Pro Met Ser Pro Ser Ser Tyr
      65              70              75              80

Phe Ala Ile Pro Pro Gly Leu Ser Pro Ala Glu Leu Leu Asp Ser Pro
      85              90              95

Val Leu Leu His Ser Ser Ser Asn Ile Leu Ala Ser Pro Thr Thr Gly
      100             105             110

Ala Ile Pro Ala Gln Arg Phe Asp Trp Lys Lys Ala Ala Asp Leu Ile
      115             120             125

Ala Ser Gln Ser Gln Gln Asp Gly Asp Ser Arg Ala Ala Ala Ala Gly
      130             135             140

Phe Asp Asp Phe Ser Phe
      145             150

```

<210> 5

<211> 1961

<212> DNA

<213> *Oryza sativa*

<400> 5

```

agtctgtctcg ttctcgtctc cgatcactct cctcctcctc ttcgtcacgg tctcctcgct 60
tcgctagctc gcttgcttgc tggctgagct gtggtacgct cgccatggcg tcctcgacgg 120
gggggttgga ccacgggttc acgttcacgc cgccgccggt catcacgtcg ttcaccgagc 180
tgctgtcggg gggcggtggg gacctgctcg gcgcggcgcg tgaggagcgc tcgccgaggg 240
ggttctccag aggcggagcg aggggtggcg gcgggggtgcc caagttcaag tccgcgcagc 300
cgccgagcct gccgtctcgc ccgcgcgcgg tgctgcgcgc gtccctacttc gccatccgcg 360
cggggtcagc ccccaaccgag ctgctcgact ccccgctcct cctcagctcc tcccatatct 420
tggcgttccc gaccaccggt gcaatcccg ctcagaggta cgactggaag gccagcgccg 480
atctcatcgc ttctcagcaa gatgacagcc gcggcgactt ctctctccac accaactccg 540
acgccatggc cgcgcaaccg gcctctttcc ctctcttcaa ggagcaagag cagcaagtgg 600
tcgagtcgag caagaacggc gccgcgcgcg cgtcgagcaa caagagcgcc ggccggcgga 660
acaacaagct ggaggacggg tacaactgga ggaagtacgg gcagaagcag gtgaagggga 720
gcgagaaccc gaggagctac tacaagtga cctacaacgg ctgctccatg aagaagaagg 780
tgagcgctc gctcgccgac ggccgcatca ccagatcgt ctacaagggc gcacacaacc 840
acccaagcc gctctccacc gcgcgaacgc ctcttccggc tccaccgccg ccgctgccc 900
cgacgacctc gcggcgcccg gcgcggcgcc ggaccagtac tccgcgcgca cgcccgagaa 960
ctctcctcgc acgttcggcg acgacgagcg cgacaacgca tcgcaccgca gcgagggcga 1020
cgagcccgaa gccaaagcgt ggaaaggagg atgctgacaa cgagggcagc tccggcgcca 1080
tgggcgggcg cgccggcgcc aaccgggtgc gcgagccgag gcttgtggtg cagacgctga 1140
gcgacatcga catcctcgac aacggcttcc ggtggaggaa gtacggccag aaggtcgtca 1200
agggaacccc caaccgaag agctactaca agtgcacgac ggtgggctgc ccggtgcca 1260
agcagctgga gcggcgctcg cacgacacgc gcgccgtgat caccacctac gagggaagc 1320
acaaccacga cgtcccggtg cgcccgcgcc ggccggcgcc gacgcgcccc ggccggcgcc 1380
tcgcctacgg ctggggggca tccggggcca cgacgctcgc cgccgcccag cagggggcct 1440
acaccctcga gatgtctccc aaccgcgcgc gcctctacgg cggctacggc gccggcgccg 1500
gcggcgccgc gttcccgccc accaaggacg agcggcgcca cgacctgttc gtcgagtcgc 1560
tcctctgcta gtcgagccga gccgagccga gctgagctgg gcccacatc cccctgctcg 1620
ccacgtggcg tattttcgcc tcgccgtata cgtacggccg tatagcgtac gtatacacgc 1680
tcgcacgcc tcgccaacac ggcaatacac acatacatac tctcgtacac acgtagtagc 1740
atacatatac agtatagtag gtggtagtgg tagctagcta gggagtgaga tccaatttgt 1800
tgattcgttg caggccactg ccacgtgggc cacaccgga acagtacacg cgtatacacc 1860
acacttgga tacgcgtacg tacgcacatg tacacgtagt tttgtgcctt tgtaactgct 1920
gagagacagg tcaataaaga ctgatgaatt tttcatttct t 1961

```

<210> 6

<211> 488

<212> PRT

<213> *Oryza sativa*

<400> 6

```

Met Ala Ser Ser Thr Gly Gly Leu Asp His Gly Phe Thr Phe Thr Pro
 1             5             10             15

Pro Pro Phe Ile Thr Ser Phe Thr Glu Leu Leu Ser Gly Gly Gly Gly
          20             25             30

Asp Leu Leu Gly Ala Gly Gly Glu Glu Arg Ser Pro Arg Gly Phe Ser
          35             40             45

Arg Gly Gly Ala Arg Val Gly Gly Gly Val Pro Lys Phe Lys Ser Ala
          50             55             60

Gln Pro Pro Ser Leu Pro Leu Ser Pro Pro Pro Val Ser Pro Ser Ser
          65             70             75             80

```

Tyr Phe Ala Ile Pro Pro Gly Leu Ser Pro Thr Glu Leu Leu Asp Ser
 85 90 95
 Pro Val Leu Leu Ser Ser Ser His Ile Leu Ala Phe Pro Thr Thr Gly
 100 105 110
 Ala Ile Pro Ala Gln Arg Tyr Asp Trp Lys Ala Ser Ala Asp Leu Ile
 115 120 125
 Ala Ser Gln Gln Asp Asp Ser Arg Gly Asp Phe Ser Phe His Thr Asn
 130 135 140
 Ser Asp Ala Met Ala Ala Gln Pro Ala Ser Phe Pro Ser Phe Lys Glu
 145 150 155 160
 Gln Glu Gln Gln Val Val Glu Ser Ser Lys Asn Gly Ala Ala Ala Ala
 165 170 175
 Ser Ser Asn Lys Ser Gly Gly Gly Gly Asn Asn Lys Leu Glu Asp Gly
 180 185 190
 Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Asn
 195 200 205
 Pro Arg Ser Tyr Tyr Lys Cys Thr Tyr Asn Gly Cys Ser Met Lys Lys
 210 215 220
 Lys Val Glu Arg Ser Leu Ala Asp Gly Arg Ile Thr Gln Ile Val Tyr
 225 230 235 240
 Lys Gly Ala His Asn His Pro Lys Pro Leu Ser Thr Ala Ala Thr Pro
 245 250 255
 Leu Pro Ala Pro Pro Pro Pro Pro Ala Pro Thr Thr Ser Arg Arg Pro
 260 265 270
 Ala Arg Ala Arg Thr Ser Thr Pro Pro Arg Arg Pro Arg Thr Pro Pro
 275 280 285
 Ser Arg Ser Ala Thr Thr Arg Pro Thr Thr His Arg Thr Ala Ala Arg
 290 295 300
 Ala Thr Ser Pro Lys Pro Ser Ala Gly Lys Glu Asp Ala Asp Asn Glu
 305 310 315 320
 Gly Ser Ser Gly Gly Met Gly Gly Gly Ala Gly Gly Asn Pro Val Arg
 325 330 335
 Glu Pro Arg Leu Val Val Gln Thr Leu Ser Asp Ile Asp Ile Leu Asp
 340 345 350
 Asn Gly Phe Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly Asn
 355 360 365
 Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Val Gly Cys Pro Val
 370 375 380
 Arg Lys His Val Glu Arg Ala Ser His Asp Thr Arg Ala Val Ile Thr
 385 390 395 400

Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Val Arg Pro Arg Arg
 405 410 415

Arg Arg Arg Thr Arg Pro Gly Ala Gly Val Ala Tyr Gly Trp Gly Arg
 420 425 430

Ser Gly Pro Thr Asp Val Ala Ala Ala Gln Gln Gly Pro Tyr Thr Leu
 435 440 445

Glu Met Leu Pro Asn Pro Ala Gly Leu Tyr Gly Gly Tyr Gly Ala Gly
 450 455 460

Ala Gly Gly Ala Ala Phe Pro Arg Thr Lys Asp Glu Arg Arg Asp Asp
 465 470 475 480

Leu Phe Val Glu Ser Leu Leu Cys
 485

<210> 7

<211> 2086

<212> DNA

<213> Oryza sativa

<400> 7

tcgtctcgtt	ctcgtctccg	atcaactctcc	tcctcatctt	cgtcacgggc	tcctcgtctc	60
gctagctcgc	ttgcttgctg	gctgagctgt	ggtacgctcg	ccatggcgtc	ctcgacgggg	120
gggttgacc	acgggttcac	gttcacgccg	ccgccgttca	tcacgtcgtt	caccgagctg	180
ctgtcggggg	gcgggtggga	cctgctcggc	gccggcggtg	aggagcgctc	gccgaggggg	240
ttctccagag	gcggagcgag	ggtgggcggc	ggggtgccca	agttcaagtc	cgcgcagccg	300
ccgagcctgc	cgctctcgcc	gccgccggtg	tcgccgtcgt	cctacttcgc	catcccgcgc	360
gggctcagcc	ccaccgagct	gctcgactcc	ccgctcctcc	tcagctcctc	ccatatcttg	420
gcgtccccga	ccaccggtgc	aatcccggct	cagaggtacg	actggaaggc	cagcgccgat	480
ctcatcgctt	ctcagcaaga	tgacagccgc	ggcgacttct	ccttccacac	caactccgac	540
gccatggccg	cgcaaccggc	ctctttccct	tccttcaagg	agcaagagca	gcaagtggtc	600
gagtcgagca	agaacggcgc	cgccgccgcg	tcgagcaaca	agagcgggcg	cggcggggaa	660
aacaagctgg	aggacgggta	caactggagg	aagtacgggc	agaagcaggt	gaaggggagc	720
gagaacccga	ggagctacta	caagtgcacc	tacaacggct	gctccatgaa	gaagaagggtg	780
gagcgctcgc	tcggccagcg	ccgcatcacc	catagctctc	acaagggcgc	acacaaccac	840
cccaagcccg	tcctccaccg	ccgcaacgcc	tcctcctgcg	ccaccgccgc	cgcctgcgcc	900
gacgacctcg	cggcgcccg	cgcgggcgcg	gaccagtact	ccgccgcgac	gcccagagaac	960
tcctccgtca	cgttcggcga	cgacgaggcc	gacaacgcac	cgcaccgcag	cgagggcgac	1020
gagcccgaag	ccaagcgctg	gaaggaggat	gctgacaacg	agggcagctc	cggcgggcatg	1080
ggcgggcgcg	ccggcgggcaa	gccggtgcgc	gagccgaggc	ttgtggtgca	gacgctgagc	1140
gacatcgaca	tcctcgacga	cggcttcggg	tggaggaagt	acggccagaa	ggtcgtcaag	1200
ggcaacccca	acccaaggag	ctactacaag	tgcacgacgg	tgggctgccc	ggtgcggaag	1260
cacgtggagc	gggcgtcgca	cgacacgcgc	gccgtgatca	ccacctacga	gggcaagcac	1320
aaccacgacg	tcccggctcg	ccgcggcgcc	ggcgggcgac	gcgccccggc	gccggcgccg	1380
ccgacgtcgg	ggcgatccg	gccgtcggcc	gtcgccgcgc	cccagcaggg	gccctacacc	1440
ctcgagatgc	tccccaaccc	cgcgcgcctc	tacggcggtc	acggcgccgc	cgcgcggcgc	1500
gccgcgttcc	cgcgcaccaa	ggacgagcgg	cgggaacgac	tggtcgtcga	gtcgtctctc	1560
tgctagtcca	gccgagccga	gccgagctga	gctgggcccc	acatccccct	gctcgccacg	1620
tggcgtattt	tcgctcggcc	gtatacgtac	ggcgtatag	cgtaactata	cacgctcgca	1680
cgcctgcccc	aacacggcaa	tacacacata	catactctcg	tacacacgta	gtagcataca	1740
tatacagtat	agtaggtggt	agtggtagct	agctagggag	tgagatccaa	tttgttgatt	1800
cgttgcaggc	cactgccacg	tgggccacac	cggaaacagt	acacgcgtat	acaccacact	1860
tgggatacgc	gtacgtacgc	acatgtacac	gtagttttgt	gcctttgtaa	ctgctgagag	1920
acaggtcaaa	taagactgat	gaatttttca	tttcttaaaa	ttccactcgt	gtgaattact	1980
agtagtataa	atatctatac	atgatgtttt	tacaactctgt	accgaactga	gaaagaggaa	2040
aaaaaagaga	gagatttttt	tttaaaaaaa	aaaaaaaaaa	aaaaaa		2086

<210> 8
 <211> 487
 <212> PRT
 <213> Oryza sativa

<400> 8
 Met Ala Ser Ser Thr Gly Gly Leu Asp His Gly Phe Thr Phe Thr Pro
 1 5 10 15
 Pro Pro Phe Ile Thr Ser Phe Thr Glu Leu Leu Ser Gly Gly Gly Gly
 20 25 30
 Asp Leu Leu Gly Ala Gly Gly Glu Arg Ser Pro Arg Gly Phe Ser
 35 40 45
 Arg Gly Gly Ala Arg Val Gly Gly Gly Val Pro Lys Phe Lys Ser Ala
 50 55 60
 Gln Pro Pro Ser Leu Pro Leu Ser Pro Pro Pro Val Ser Pro Ser Ser
 65 70 75 80
 Tyr Phe Ala Ile Pro Pro Gly Leu Ser Pro Thr Glu Leu Leu Asp Ser
 85 90 95
 Pro Val Leu Leu Ser Ser Ser His Ile Leu Ala Ser Pro Thr Thr Gly
 100 105 110
 Ala Ile Pro Ala Gln Arg Tyr Asp Trp Lys Ala Ser Ala Asp Leu Ile
 115 120 125
 Ala Ser Gln Gln Asp Asp Ser Arg Gly Asp Phe Ser Phe His Thr Asn
 130 135 140
 Ser Asp Ala Met Ala Ala Gln Pro Ala Ser Phe Pro Ser Phe Lys Glu
 145 150 155 160
 Gln Glu Gln Gln Val Val Glu Ser Ser Lys Asn Gly Ala Ala Ala Ala
 165 170 175
 Ser Ser Asn Lys Ser Gly Gly Gly Gly Asn Asn Lys Leu Glu Asp Gly
 180 185 190
 Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Asn
 195 200 205
 Pro Arg Ser Tyr Tyr Lys Cys Thr Tyr Asn Gly Cys Ser Met Lys Lys
 210 215 220
 Lys Val Glu Arg Ser Leu Ala Asp Gly Arg Ile Thr Gln Ile Val Tyr
 225 230 235 240
 Lys Gly Ala His Asn His Pro Lys Pro Leu Ser Thr Arg Arg Asn Ala
 245 250 255
 Ser Ser Cys Ala Thr Ala Ala Ala Cys Ala Asp Asp Leu Ala Ala Pro
 260 265 270

Gly Ala Gly Ala Asp Gln Tyr Ser Ala Ala Thr Pro Glu Asn Ser Ser
 275 280 285
 Val Thr Phe Gly Asp Asp Glu Ala Asp Asn Ala Ser His Arg Ser Glu
 290 295 300
 Gly Asp Glu Pro Glu Ala Lys Arg Trp Lys Glu Asp Ala Asp Asn Glu
 305 310 315 320
 Gly Ser Ser Gly Gly Met Gly Gly Gly Ala Gly Gly Lys Pro Val Arg
 325 330 335
 Glu Pro Arg Leu Val Val Gln Thr Leu Ser Asp Ile Asp Ile Leu Asp
 340 345 350
 Asp Gly Phe Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly Asn
 355 360 365
 Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Val Gly Cys Pro Val
 370 375 380
 Arg Lys His Val Glu Arg Ala Ser His Asp Thr Arg Ala Val Ile Thr
 385 390 395 400
 Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Val Gly Arg Gly Gly
 405 410 415
 Gly Gly Gly Arg Ala Pro Ala Pro Ala Pro Pro Thr Ser Gly Ala Ile
 420 425 430
 Arg Pro Ser Ala Val Ala Ala Ala Gln Gln Gly Pro Tyr Thr Leu Glu
 435 440 445
 Met Leu Pro Asn Pro Ala Gly Leu Tyr Gly Gly Tyr Gly Ala Gly Ala
 450 455 460
 Gly Gly Ala Ala Phe Pro Arg Thr Lys Asp Glu Arg Arg Asp Asp Leu
 465 470 475 480
 Phe Val Glu Ser Leu Leu Cys
 485

<210> 9

<211> 1928

<212> DNA

<213> Glycine max

<400> 9

gcacgagtct	catggcatct	tcttctggta	gtttagacac	ctctgcaagt	gcaaaactcct	60
tcaccaactt	caccttctcc	acacaccctt	tcatgaccac	ttctttctct	gacctccttg	120
cttctccctt	ggacaacaac	aagccaccac	agggtggttt	gtctgagaga	actggctctg	180
gtgttcccaa	attcaagtcc	acaccaccac	cttctctgcc	tctctctccc	cctcccattt	240
ctccttcttc	ttactttgct	attcctcctg	gtttgagccc	tgctgagctt	cttgactcgc	300
cggttctcct	taactcttcc	aacattctgc	catctccaac	aactggagca	tttgttgctc	360
agagcttcaa	ttggaagagc	agttcagggg	ggaatcagca	aattgtcaag	gaagaagaca	420
aaagcttctc	aaatttctct	ttccaaaccc	gatcaggacc	tcctgcttca	tccacagcaa	480
cataccagtc	ttcaaagtgc	acagttcaaa	cacaacagcc	atggagtttt	caggaggcca	540
cgaacagga	taatttttcc	tcaggaaagg	gtatgatgaa	aactgaaaac	tcttcttcca	600
tgcagagttt	ttcccctgag	attgctagtg	tccaaactaa	ccatagcaat	gggtttcaat	660

```

ccgattatgg caattacccc ccacaatctc agactttaag tagaagggtca gatgatgggt 720
acaattggag gaaatatggc caaaaacaag tgaagggaag tgaaaatcca agaagttatt 780
acaaatgcac ataccccacat tgccctacaa agaagaaggt tgagagggtct ttagatggac 840
aaattactga gatagtttat aagggtactc ataaccatcc taagcctcaa aatactagga 900
gaaactcatc aaactcctct tctcttgcaa tccctcattc aaattccatc agaactgaaa 960
tcccagatca atcctatgcc acacatggaa gtggacaaat ggattcagct gccaccccag 1020
aaaactcatc aatatcaatt ggagatgatg attttgagca gagttcccaa aagtgtaaat 1080
caggagggga tgaatatgat gaagatgaac ctgatgccaa aagatggaaa attgaagggtg 1140
aaaatgaggg tatgtcagcc cctggaagta gaacagttag agaacctaga gttgtagtct 1200
agacaaccag tgacattgat atccttgatg atggctatag gtggagaaaa tacgggcaga 1260
aagtagtgaa gggcaatcca aatccaagga gttactacaa gtgcacacac ccaggatgtc 1320
cagttaggaa gcacgtggaa agagcctcac atgacctaa ggctgtgatc acaacttatg 1380
agggaaagca caaccatgat gttcctgcag cccgtggcag tggcagccat tctgtgaaca 1440
gaccaatgcc aaacaatgct tcaaaccaca ccaacactgc agccacttcc gtaagggtct 1500
tgccagtgat ccaccaaagt gacaattccc ttcagaacca aagatcacao gcaccaccag 1560
aagggcaatc acccttcacc ctagagatgc tacaaagtcc aggaagtttt ggattctcag 1620
ggtttgaggaa tccaatgcaa tcttacgtga accagcagca actatctgac aatgttttct 1680
cctccaggac caaggaggag cctagagatg acatgttcct tgagtctcta ctatgctgaa 1740
ggaatttttt ttttcccttt ttggtagcta tgggaaggttg gaaatttttg aagtggggga 1800
ctaggattta ttggacaaat aaggttccat tcgatttatt gcattttttg gtttgttttg 1860
ttgtaaattt tatacagcca caggattggt atagtatata ctagtatttc aaaaaaaaaa 1920
aaaaaaaaa 1928

```

<210> 10

<211> 575

<212> PRT

<213> Glycine max

<400> 10

```

Met Ala Ser Ser Ser Gly Ser Leu Asp Thr Ser Ala Ser Ala Asn Ser
  1              5              10              15

```

```

Phe Thr Asn Phe Thr Phe Ser Thr His Pro Phe Met Thr Thr Ser Phe
      20              25              30

```

```

Ser Asp Leu Leu Ala Ser Pro Leu Asp Asn Asn Lys Pro Pro Gln Gly
      35              40              45

```

```

Gly Leu Ser Glu Arg Thr Gly Ser Gly Val Pro Lys Phe Lys Ser Thr
      50              55              60

```

```

Pro Pro Pro Ser Leu Pro Leu Ser Pro Pro Pro Ile Ser Pro Ser Ser
      65              70              75              80

```

```

Tyr Phe Ala Ile Pro Pro Gly Leu Ser Pro Ala Glu Leu Leu Asp Ser
      85              90              95

```

```

Pro Val Leu Leu Asn Ser Ser Asn Ile Leu Pro Ser Pro Thr Thr Gly
      100              105              110

```

```

Ala Phe Val Ala Gln Ser Phe Asn Trp Lys Ser Ser Ser Gly Gly Asn
      115              120              125

```

```

Gln Gln Ile Val Lys Glu Glu Asp Lys Ser Phe Ser Asn Phe Ser Phe
      130              135              140

```

```

Gln Thr Arg Ser Gly Pro Pro Ala Ser Ser Thr Ala Thr Tyr Gln Ser
      145              150              155              160

```

Ser Asn Val Thr Val Gln Thr Gln Gln Pro Trp Ser Phe Gln Glu Ala
 165 170 175
 Thr Lys Gln Asp Asn Phe Ser Ser Gly Lys Gly Met Met Lys Thr Glu
 180 185 190
 Asn Ser Ser Ser Met Gln Ser Phe Ser Pro Glu Ile Ala Ser Val Gln
 195 200 205
 Thr Asn His Ser Asn Gly Phe Gln Ser Asp Tyr Gly Asn Tyr Pro Pro
 210 215 220
 Gln Ser Gln Thr Leu Ser Arg Arg Ser Asp Asp Gly Tyr Asn Trp Arg
 225 230 235 240
 Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Asn Pro Arg Ser Tyr
 245 250 255
 Tyr Lys Cys Thr Tyr Pro Asn Cys Pro Thr Lys Lys Lys Val Glu Arg
 260 265 270
 Ser Leu Asp Gly Gln Ile Thr Glu Ile Val Tyr Lys Gly Thr His Asn
 275 280 285
 His Pro Lys Pro Gln Asn Thr Arg Arg Asn Ser Ser Asn Ser Ser Ser
 290 295 300
 Leu Ala Ile Pro His Ser Asn Ser Ile Arg Thr Glu Ile Pro Asp Gln
 305 310 315 320
 Ser Tyr Ala Thr His Gly Ser Gly Gln Met Asp Ser Ala Ala Thr Pro
 325 330 335
 Glu Asn Ser Ser Ile Ser Ile Gly Asp Asp Asp Phe Glu Gln Ser Ser
 340 345 350
 Gln Lys Cys Lys Ser Gly Gly Asp Glu Tyr Asp Glu Asp Glu Pro Asp
 355 360 365
 Ala Lys Arg Trp Lys Ile Glu Gly Glu Asn Glu Gly Met Ser Ala Pro
 370 375 380
 Gly Ser Arg Thr Val Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser
 385 390 395 400
 Asp Ile Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln
 405 410 415
 Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr
 420 425 430
 His Pro Gly Cys Pro Val Arg Lys His Val Glu Arg Ala Ser His Asp
 435 440 445
 Leu Arg Ala Val Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp Val
 450 455 460
 Pro Ala Ala Arg Gly Ser Gly Ser His Ser Val Asn Arg Pro Met Pro
 465 470 475 480

WO 01/49840

PCT/US00/35310

Asn Asn Ala Ser Asn His Thr Asn Thr Ala Ala Thr Ser Val Arg Leu
485 490 495

Leu Pro Val Ile His Gln Ser Asp Asn Ser Leu Gln Asn Gln Arg Ser
500 505 510

Gln Ala Pro Pro Glu Gly Gln Ser Pro Phe Thr Leu Glu Met Leu Gln
515 520 525

Ser Pro Gly Ser Phe Gly Phe Ser Gly Phe Gly Asn Pro Met Gln Ser
530 535 540

Tyr Val Asn Gln Gln Gln Leu Ser Asp Asn Val Phe Ser Ser Arg Thr
545 550 555 560

Lys Glu Glu Pro Arg Asp Asp Met Phe Leu Glu Ser Leu Leu Cys
565 570 575

<210> 11
<211> 2158
<212> DNA
<213> Triticum aestivum

<400> 11

gcacgagccg	caccgcgccc	atggccgatt	cgccaaaccc	tagctccggg	gacctcccct	60
cagccgcccg	gagctcgccc	gagaagccgt	accccgccga	tcgacgcgtc	gcggcgctcg	120
ccggcgccgg	cgcgaggtac	aaggccatgt	ccccggcgcg	gctgccgatc	tcgcgcgagc	180
cctgcctcac	catccccgcc	ggcttcagcc	cctccgccct	cctcgactcc	cccgtgctcc	240
tcaccaactt	caaggttgaa	ccttcaccaa	caactggtag	tctgagcatg	gctgcaatta	300
tgcacaagag	tgctcatcca	gacatactgc	cttcgccacg	ggataagtct	attcgagccc	360
atgaagatgg	gggttctagg	gattttgaat	tcaagcctca	tctgaattcg	tcttctcaat	420
cactggctcc	tgctatgagt	gatctaataa	aacacgagca	ttctatgcaa	aatcagagta	480
tgaatcccag	ctcatcatct	agcaatatgg	tgaatgaaaa	cagacctccc	tggttcacgcg	540
agtcaagtct	tacagtgaat	gtaagtgtct	cgaaccaacc	tggttggaatg	gttggtttga	600
ctgacaacat	gcctgctgaa	gttggtacat	ctgagccgca	gcagatgaat	agttctgaca	660
atgccatgca	agagccgcag	tctgaaaatg	ttgctgacaa	gtcagcagat	gatggctaca	720
actggcgcaa	atatgggcag	aagcatgtca	agggaaagtga	aaaccctaga	agttattaca	780
agtgacacaa	tcctaattgt	gaagtaaaaa	agctatttga	gcgtgcgggt	gatggtctga	840
tcacgggaagt	tgctataaag	ggcgcccata	atcatcctaa	gccccagcct	aataggaggt	900
tagctgggtg	tgcaagttcc	tcgaaccagg	gtgaagaacg	atatgatggg	gcggcgagctg	960
ctgatgataa	atcttccaat	gctcttagca	accttgctaa	tcgggtaaat	tcgcctggca	1020
tggttgagcc	tggtccagtt	tcagtttagt	atgatgacat	agatgctgga	gggtggaagac	1080
cctaccctgg	ggatgatgct	acagaggagg	atttagagtc	gaaacgcagg	aaaatggagt	1140
ctgcagggtat	tgatgctgct	ctgatgggta	aacctaaccc	tgagccccgt	gttgtcgttc	1200
agactgtaag	tgagggtgac	atcttggtat	atgggtatcg	ttggcggaag	tatggacaga	1260
aagttgtcaa	aggaaacccc	aatccacgga	gttactacaa	atgcacaagc	acaggatgcc	1320
ctgtgaggaa	gcaggttgag	agagcatcgc	acgatcctaa	atcagtgata	acaacgtatg	1380
aaggaaaaca	taaccatgaa	gtccctgctg	cgaggaatgc	aacctatgag	atgtccgcgc	1440
ctcccatgaa	gaatgtcgtg	catcagatta	acagcagtat	gcccagcagc	attggcgcca	1500
tgatgagagc	atgtgaagcc	aggaacttca	gcaaccaata	ttctcaagcc	gctgaaaccc	1560
acaatgtcag	tcttgacctt	ggtgttgga	tcagcccga	ccacagcgat	gccacaaacc	1620
aaatgcagtc	ttcaggtcct	gatcagatgc	agtaccagat	gcaatccatg	gcttcgatgt	1680
acggcaacat	gagacatcca	tcataaatgg	cagtgccaac	ggtacaagga	aactctgctg	1740
gccgcatgta	tggttccaga	gaagagaaag	gtaacgaagg	gtttactttc	agagccacac	1800
cgatggacca	ttcagctaac	ctatgctata	gcgggtgctg	gaacttggtc	atgggtccat	1860
gagaggaatg	atgagagtgt	cagcaaatgc	ttatagctcc	atgaatcata	tattacaaac	1920
aatgcttttg	taacgacaat	ctcttcagca	agattcttaa	ttgtgtatcg	gttacaagtc	1980
agttcagcca	gaggcaagta	agctataagc	tatacctgga	ggactgcagc	aatgcgcgat	2040

gtgtcttttt aggcgcggaa aaggccctg ctgtatgtag cgtgcagac ctacattcgt 2100
 tgtacagcga acctaataatg attaattaat tagattatga gaatttggtt taaaaaaaa 2158

<210> 12
 <211> 619
 <212> PRT
 <213> Triticum aestivum

<400> 12
 Thr Ser Arg Thr Ala Pro Met Ala Asp Ser Pro Asn Pro Ser Ser Gly
 1 5 10 15
 Asp Leu Pro Ser Ala Ala Gly Ser Ser Pro Glu Lys Pro Tyr Pro Ala
 20 25 30
 Asp Arg Arg Val Ala Ala Leu Ala Gly Ala Gly Ala Arg Tyr Lys Ala
 35 40 45
 Met Ser Pro Ala Arg Leu Pro Ile Ser Arg Glu Pro Cys Leu Thr Ile
 50 55 60
 Pro Ala Gly Phe Ser Pro Ser Ala Leu Leu Asp Ser Pro Val Leu Leu
 65 70 75 80
 Thr Asn Phe Lys Val Glu Pro Ser Pro Thr Thr Gly Ser Leu Ser Met
 85 90 95
 Ala Ala Ile Met His Lys Ser Ala His Pro Asp Ile Leu Pro Ser Pro
 100 105 110
 Arg Asp Lys Ser Ile Arg Ala His Glu Asp Gly Gly Ser Arg Asp Phe
 115 120 125
 Glu Phe Lys Pro His Leu Asn Ser Ser Ser Gln Ser Leu Ala Pro Ala
 130 135 140
 Met Ser Asp Leu Lys Lys His Glu His Ser Met Gln Asn Gln Ser Met
 145 150 155 160
 Asn Pro Ser Ser Ser Ser Ser Asn Met Val Asn Glu Asn Arg Pro Pro
 165 170 175
 Cys Ser Arg Glu Ser Ser Leu Thr Val Asn Val Ser Ala Pro Asn Gln
 180 185 190
 Pro Val Gly Met Val Gly Leu Thr Asp Asn Met Pro Ala Glu Val Gly
 195 200 205
 Thr Ser Glu Pro Gln Gln Met Asn Ser Ser Asp Asn Ala Met Gln Glu
 210 215 220
 Pro Gln Ser Glu Asn Val Ala Asp Lys Ser Ala Asp Asp Gly Tyr Asn
 225 230 235 240
 Trp Arg Lys Tyr Gly Gln Lys His Val Lys Gly Ser Glu Asn Pro Arg
 245 250 255
 Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys Glu Val Lys Lys Leu Leu
 260 265 270

Glu Arg Ala Val Asp Gly Leu Ile Thr Glu Val Val Tyr Lys Gly Arg
 275 280 285
 His Asn His Pro Lys Pro Gln Pro Asn Arg Arg Leu Ala Gly Gly Ala
 290 295 300
 Val Pro Ser Asn Gln Gly Glu Glu Arg Tyr Asp Gly Ala Ala Ala Ala
 305 310 315 320
 Asp Asp Lys Ser Ser Asn Ala Leu Ser Asn Leu Ala Asn Pro Val Asn
 325 330 335
 Ser Pro Gly Met Val Glu Pro Val Pro Val Ser Val Ser Asp Asp Asp
 340 345 350
 Ile Asp Ala Gly Gly Gly Arg Pro Tyr Pro Gly Asp Asp Ala Thr Glu
 355 360 365
 Glu Asp Leu Glu Ser Lys Arg Arg Lys Met Glu Ser Ala Gly Ile Asp
 370 375 380
 Ala Ala Leu Met Gly Lys Pro Asn Arg Glu Pro Arg Val Val Val Gln
 385 390 395 400
 Thr Val Ser Glu Val Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys
 405 410 415
 Tyr Gly Gln Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr
 420 425 430
 Lys Cys Thr Ser Thr Gly Cys Pro Val Arg Lys His Val Glu Arg Ala
 435 440 445
 Ser His Asp Pro Lys Ser Val Ile Thr Thr Tyr Glu Gly Lys His Asn
 450 455 460
 His Glu Val Pro Ala Ala Arg Asn Ala Thr His Glu Met Ser Ala Pro
 465 470 475 480
 Pro Met Lys Asn Val Val His Gln Ile Asn Ser Ser Met Pro Ser Ser
 485 490 495
 Ile Gly Gly Met Met Arg Ala Cys Glu Ala Arg Asn Phe Ser Asn Gln
 500 505 510
 Tyr Ser Gln Ala Ala Glu Thr Asp Asn Val Ser Leu Asp Leu Gly Val
 515 520 525
 Gly Ile Ser Pro Asn His Ser Asp Ala Thr Asn Gln Met Gln Ser Ser
 530 535 540
 Gly Pro Asp Gln Met Gln Tyr Gln Met Gln Ser Met Ala Ser Met Tyr
 545 550 555 560
 Gly Asn Met Arg His Pro Ser Ser Met Ala Val Pro Thr Val Gln Gly
 565 570 575
 Asn Ser Ala Gly Arg Met Tyr Gly Ser Arg Glu Glu Lys Gly Asn Glu
 580 585 590

15

Pro Thr Lys Lys Lys Val Glu Arg Ala Leu Asp Gly Gln Ile Thr Glu
 245 250 255
 Ile Val Tyr Lys Gly Ala His Asn His Pro Lys Pro Gln Ser Thr Arg
 260 265 270
 Arg Ser Ser Ser Ser Thr Ala Ser Ser Ala Ser Thr Leu Ala Ala Gln
 275 280 285
 Ser Tyr Asn Ala Pro Ala Ser Asp Val Pro Asp Gln Ser Tyr Trp Ser
 290 295 300
 Asn Gly Asn Gly Gln Met Asp Ser Val Ala Thr Pro Glu Asn Ser Ser
 305 310 315 320
 Ile Ser Val Gly Asp Asp Glu Phe Glu Gln Ser Ser Gln Lys Arg Glu
 325 330 335
 Ser Gly Gly Asp Glu Phe Asp Glu Asp Glu Pro Asp Ala Lys Arg Trp
 340 345 350
 Lys Val Glu Asn Glu Ser Glu Gly Val Ser Ala Gln Gly Ser Arg Thr
 355 360 365
 Val Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser Asp Ile Asp Ile
 370 375 380
 Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys
 385 390 395 400
 Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ser Gln Gly Cys
 405 410 415
 Pro Val Arg Lys His Val Glu Arg Ala Ser His Asp Ile Arg Ser Val
 420 425 430
 Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Ala Ala Arg
 435 440 445
 Gly Ser Gly Ser His Gly Leu Asn Arg Gly Ala Asn Pro Asn Asn Asn
 450 455 460
 Ala Ala Met Ala Met Ala Ile Arg Pro Ser Thr Met Ser Leu Gln Ser
 465 470 475 480
 Asn Tyr Pro Ile Pro Ile Pro Ser Thr Arg Pro Met Gln Gln Gly Glu
 485 490 495
 Gly Gln Ala Pro Tyr Glu Met Leu Gln Gly Ser Gly Gly Phe Gly Tyr
 500 505 510
 Ser Gly Phe Gly Asn Pro Met Asn Ala Tyr Ala Asn Gln Ile Gln Asp
 515 520 525
 Asn Ala Phe Ser Arg Ala Lys Glu Glu Pro Arg Asp Asp Leu Phe Leu
 530 535 540
 Asp Thr Leu Leu Ala
 545

WO 01/49840

PCT/US00/35310

<210> 14
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Synthetic oligonucleotide
 <400> 14
 gaaaaattca tcagtggatc cttatttgac ctgtct 36